

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Yi Sun
(B) STREET: 4841 Hillway Court
(C) CITY: Ann Arbor
(D) STATE: Michigan
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 48105
(G) TELEPHONE: (313) 996-1959
(H) TELEFAX: (313) 996-7158

(ii) TITLE OF INVENTION: Sensitive to Apoptosis Gene (SAG)

(iii) NUMBER OF SEQUENCES: 50

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:17..355

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:17..355

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:1..1140
(D) OTHER INFORMATION:/note= "Mouse SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC 49
 Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys
 1 5 10

 GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC 97
 Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp
 15 20 25

 AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG 145
 Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp
 30 35 40

 GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT 193
 Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp
 45 50 55

 GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG 241
 Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val
 60 65 70 75

 GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG 289
 Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu
 80 85 90

TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA	337
Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val	
95 100 105	
GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG	385
Val Gln Arg Ile Gly Lys	
110	
TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT	445
GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTGG	505
GAAATTCTCT ACAATTAAGA TAATTTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT	565
GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC	625
CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTATTATGCT TGAGGGTTAA	685
AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT	745
AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG	805
AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG	865
GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA	925
AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG	985
TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG	1045
TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC	1105
TCTTAAAATC ATTAAACTAA TTCATCAATT AAATG	1140

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Pro	Cys	Val	Leu	Ser	Ser	His
1				5					10					15	
Ser	Gly	Ser	Ala	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp
		35					40					45			
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys
	50					55				60					
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys
65				70					75					80	
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn
			85					90					95		
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
		100						105					110		

Lys

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:1..754
(D) OTHER INFORMATION:/note= "Human SAG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAAGAG CCCTGGTGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1 5 10 15
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 20 25 30
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 35 40 45
 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50 55 60
 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
 65 70 75 80
 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
 85 90 95
 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
 100 105 110
 Lys

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide P1 downstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTTTTT TTTTTTTR

18

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide: P2 upstream primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCTTNNNN NNN

13

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGGGATCCCC ATGCCGACG TGAGG

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CGGGATCCTC ATTTGCCGAT TCTTTG

26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide P.01"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TATGGCTAGC ATGCCGACG TGGAGG

26

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln	Asn	Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..270

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG ATG CCT GTC TTA GAT GTC AAG CTG	192
Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu	
50 55 60	
AAA ACA AAC AAG AGG ACT GTG TTG TGG TCT GGG GAG AAT GTA ATC ATT	240
Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile	
65 70 75 80	
CCT TCC ACA ACT GCT GCA TGT CCC TGT GGG TGAAACAGAA CAATCGCTGC	290
Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly	
85 90	
CCTCTCTGCC AGCAGGACTG GGTGGTCCAA AGAATCGGCA AATGAGAGTG GTTAGAAGGC	350
TTCTTAGCGC AGTTGTTTCAG AGCCCTGGTG GATCTTGTA TCCAGTGCCC TACAAAGGCT	410
AGAACACTAC AGGGGATGAA TTCTTCAAAT AGGAGCCGAT GGATCTGTGG TCTTTGACT	470
CATCAAAGCC TTGGTTAGCA TTTGTCAGTT TTATCTTCAG AAATTCTCTG TGATTAAGAA	530
GATAATTTAT TAAAGGTGGT CCTTCCTACC TCTGTGGTGT GTGTCGCGCA CACAGCTTAG	590
AAGTGCTATA AAAAAGGAAA GAGCTCCAAA TTGAATCACC TTATAATTTA CCCATTTCTA	650
TACAACAGGC AGTGAAGCA GTTTCGAGAC TTTTTCGATG CTTATGGTTG ATCAGTTAAA	710
AAAGAATGTT ACAGTAACAA ATAAAGTGCA GTTTAAA	747

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Cys Ala Ile Cys Arg Val Gln Met Pro Val Leu Asp Val Lys Leu
50 55 60
Lys Thr Asn Lys Arg Thr Val Leu Trp Ser Gly Glu Asn Val Ile Ile
65 70 75 80
Pro Ser Thr Thr Ala Ala Cys Pro Cys Gly
85 90

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..291

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GTG GTC TGG GGA GAA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys	
50 55 60	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	240
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
65 70 75 80	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	288
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
85 90 95	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	341
Lys	
TCTTGTAATC CAGTGCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	401
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	461
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	521
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	581
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	641
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	701
TTAAA	706

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His

1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	20	25	30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	35	40	45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Val Val Trp Gly Glu Cys	50	55	60
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	65	70	75
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	85	90	95

Lys

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide hSAG. M1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCATCTGCA GGGTCCAG

18

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02L"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCTCAT TTGCCGATTC TTTGGAC

27

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide SAGKanMX4-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCCAGTG GCAGAGAACT TTAAAGAGAA ATAGTTCAAC CGTACGCTGC AGGTCGAC

58

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide SAGKan MX
 4-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 ACCTCGGTAT GATTTAAATG TTTACGGGCA ATTCATTTTT ATCGATGAAT TCGAGCTCG 59

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 TTCTCCAGTG GCAGAGAAC 19

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide SAG pcr 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 ATGATTTAAA TGTTTACGGG C 21

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..339

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG AGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGG	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Ser Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly

Lys

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..339

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCTTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCCGCGACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1           5           10           15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
          20           25           30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
          35           40           45
Thr Cys Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
          50           55           60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
          65           70           75           80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
          85           90           95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
          100          105          110
Lys
```

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1           5           10           15
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
          20           25           30
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT     144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
          35           40           45
ACG AGC GCC ATC AGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT     192
Thr Ser Ala Ile Ser Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
          50           55           60
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT     240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
          65           70           75           80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC     288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
```

85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC			336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly			
100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA			389
Lys			
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG			449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT			509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC			569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT			629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGAAGCAGT TTCGAGACTT			689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT			749
TTAAA			754

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1				5					10					15	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp
		35				40						45			
Thr	Ser	Ala	Ile	Ser	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys
	50					55				60					
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys
65				70					75					80	
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn
			85					90					95		
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
		100						105				110			
Lys															

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Cys	
50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	

Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110

Lys

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA AGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1           5           10           15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
          20           25           30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
          35           40           45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
          50           55           60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Ser
          65           70           75           80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
          85           90           95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
          100          105          110
Lys

```

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1           5           10           15
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
          20           25           30
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT     144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
          35           40           45
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT     192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
          50           55           60
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT     240

```


Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys		
65					70					75					80		
AAT	AAA	TCC	TTC	CAC	AAC	TGC	TGC	ATG	TCC	CTG	TGG	GTG	AAA	CAG	AAC		288
Asn	Lys	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
				85					90					95			
AAT	CGC	TGC	CCT	CTC	TGC	CAG	CAG	GAC	TGG	GTG	GTC	CAA	AGA	ATC	GGC		336
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly		
			100					105						110			
AAA	TGAGAGTGGT	TAGAAGGCTT	CTTAGCGCAG	TTGTTTCAGAG	CCCTGGTGGA												389
Lys																	
TCTTGTAATC	CAGTGCCCTA	CAAAGGCTAG	AACACTACAG	GGGATGAATT	CTTCAAATAG												449
GAGCCGATGG	ATCTGTGGTC	TTTGGACTCA	TCAAAGCCTT	GGTTAGCATT	TGTCAGTTTT												509
ATCTTCAGAA	ATTCTCTGTG	ATTAAGAAGA	TAATTTATTA	AAGGTGGTCC	TTCCTACCTC												569
TGTGGTGTGT	GTCGCGCACA	CAGCTTAGAA	GTGCTATAAA	AAAGGAAAGA	GCTCCAAATT												629
GAATCACCTT	ATAATTTACC	CATTTCTATA	CAACAGGCAG	TGGAAGCAGT	TCGAGACTT												689
TTTCGATGCT	TATGGTTGAT	CAGTTAAAAA	AGAATGTTAC	AGTAACAAAT	AAAGTGCAGT												749
TTAAA																	754

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His		
1				5					10					15			
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu		
			20					25					30				
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp		
		35					40					45					
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys		
		50				55					60						
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys		
65					70					75					80		
Asn	Lys	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn		
				85					90					95			
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly		
			100					105						110			
Lys																	

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCTAGAG CCCTGGTGGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn His Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC AGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Ser Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCTTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629

GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1				5					10					15	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp
		35					40					45			
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Cys
	50					55					60				
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys
65					70					75				80	
Asn	His	Ser	Phe	His	Asn	Cys	Ser	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn
				85					90					95	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
		100						105					110		

Lys

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATG	GCC	GAC	GTG	GAA	GAC	GGA	GAG	GAA	ACC	TGC	GCC	CTG	GCC	TCT	CAC
Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1				5					10					15	
TCC	GGG	AGC	TCA	GGC	TCC	AAG	TCG	GGA	GGC	GAC	AAG	ATG	TTC	TCC	CTC
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		
AAG	AAG	TGG	AAC	GCG	GTG	GCC	ATG	TGG	AGC	TGG	GAC	GTG	GAG	TGC	GAT
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp
		35					40					45			

ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC AGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
Asn Arg Ser Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
Lys	

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT AAA TCC TTC AAG AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCACT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	

20	25	30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp		
35	40	45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys		
50	55	60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys		
65	70	75
Asn Lys Ser Phe Lys Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn		
85	90	95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly		
100	105	110

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..339

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48.
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA AGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Ser	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGGCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449

GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met	Ala	Asp	Val	Glu	Asp	Gly	Glu	Glu	Thr	Cys	Ala	Leu	Ala	Ser	His
1				5					10					15	
Ser	Gly	Ser	Ser	Gly	Ser	Lys	Ser	Gly	Gly	Asp	Lys	Met	Phe	Ser	Leu
			20					25					30		
Lys	Lys	Trp	Asn	Ala	Val	Ala	Met	Trp	Ser	Trp	Asp	Val	Glu	Cys	Asp
		35					40					45			
Thr	Cys	Ala	Ile	Cys	Arg	Val	Gln	Val	Met	Asp	Ala	Cys	Leu	Arg	Ser
	50					55				60					
Gln	Ala	Glu	Asn	Lys	Gln	Glu	Asp	Cys	Val	Val	Val	Trp	Gly	Glu	Cys
	65				70					75					80
Asn	His	Ser	Phe	His	Asn	Cys	Cys	Met	Ser	Leu	Trp	Val	Lys	Gln	Asn
				85					90					95	
Asn	Arg	Cys	Pro	Leu	Cys	Gln	Gln	Asp	Trp	Val	Val	Gln	Arg	Ile	Gly
			100					105					110		

Lys

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	

AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC AGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA	389
Lys	
TCTTGTAATC CAGTGCCTTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
Gln Ala Glu Asn Lys Gln Glu Asp Ser Val Val Val Trp Gly Glu Cys	
65 70 75 80	
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
Lys	

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..339

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC AGT CTT AGA AGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGG	389
Lys	
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG	449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT	509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC	569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT	629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGAAGCAGT TTCGAGACTT	689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT	749
TTAAA	754

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
1 5 10 15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
20 25 30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
35 40 45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Ser Leu Arg Ser
50 55 60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65 70 75 80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
85 90 95
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..339

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC	48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	
1 5 10 15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC	96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	
20 25 30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT	144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp	
35 40 45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT	192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	
50 55 60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT	240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	
65 70 75 80	
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC	288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	
85 90 95	
AAT CGC AGC CCT CTC AGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC	336
Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly	
100 105 110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTCAGAG CCCTGGTGGA	389

Lys

```
TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG 449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT 509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC 569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT 629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT 689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT 749
TTAAA 754
```

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 1             5             10             15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
          20             25             30
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
          35             40             45
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
 50             55             60
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
65             70             75             80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
          85             90             95
Asn Arg Ser Pro Leu Ser Gln Gln Asp Trp Val Val Gln Arg Ile Gly
100             105             110
```

Lys

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC 48
Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
```

1	5	10	15	
TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC				96
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	20	25	30	
AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG AGC GAT				144
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp	35	40	45	
ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT				192
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60	
CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT				240
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	65	70	75	80
AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC				288
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95	
AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC				336
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110	
AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA				389
Lys				
TCTTGTAATC CAGTGGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG				449
GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTT				509
ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCTTACCTC				569
TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT				629
GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT				689
TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT				749
TTAAA				754

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His	1	5	10	15
Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu	20	25	30	
Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Ser Asp	35	40	45	
Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys	50	55	60	
Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys	65	70	75	80
Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn	85	90	95	
Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly	100	105	110	

Lys

ad
cont

